

SEQUENCE LISTING

<110> Innovations Foundation

<120> Recombinant BCG Strains Expressing Alanine Dehydrogenase,
Serine dehydratase and/or Glutamine Synthetase as TB Vaccines

<130>

<150> US 60/372,450

<151> 2002-04-16

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 1116

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1116)

<223> Sequence is identical to GenBank entries GI:3089350 and MTU92472

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48

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Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
20 25 30

96

gtg ctc atc cag gca ggt gcc gga gag ggc tcg gct atc acc gac gcg
Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45

144

gat ttc aag gcg gca ggc gcg caa ctg gtc ggc acc gcc gac cag gtg
Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60

192

tgg gcc gac gct gat tta ttg ctc aag gtc aaa gaa ccg ata gcg gcg
Trp Ala Asp Ala Asp Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80

240

gaa tac ggc cgc ctg cga cac ggg cag atc ttg ttc acg ttc ttg cat
Glu Tyr Gly Arg Leu Arg His Gly Gln Ile Leu Phe Thr Phe Leu His
85 90 95

288

ttg gcc gcg tca cgt gct tgc acc gat gcg ttg ttg gat tcc ggc acc
Leu Ala Ala Ser Arg Ala Cys Thr Asp Ala Leu Leu Asp Ser Gly Thr
100 105 110

336

acg tca att gcc tac gag acc gtc cag acc gcc gac ggc gca cta ccc

384

Thr Ser Ile Ala Tyr Glu Thr Val Gln Thr Ala Asp Gly Ala Leu Pro			
115	120	125	
ctg ctt gcc ccg atg agc gaa gtc gcc ggt cga ctc gcc gcc cag gtt			432
Leu Leu Ala Pro Met Ser Glu Val Ala Gly Arg Leu Ala Ala Gln Val			
130	135	140	
ggc gct tac cac ctg atg cga acc caa ggg ggc cgc ggt gtg ctg atg			480
Gly Ala Tyr His Leu Met Arg Thr Gln Gly Arg Gly Val Leu Met			
145	150	155	160
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Gly Gly Val Pro Gly Val Glu Pro Ala Asp Val Val Val Ile Gly Ala			
165	170	175	
ggc acc gcc ggc tac aac gca gcc cgc atc gcc aac ggc atg ggc gcg			576
Gly Thr Ala Gly Tyr Asn Ala Ala Arg Ile Ala Asn Gly Met Gly Ala			
180	185	190	
acc gtt acg gtt cta gac atc aac atc gac aaa ctt cgg caa ctc gac			624
Thr Val Thr Val Leu Asp Ile Asn Ile Asp Lys Leu Arg Gln Leu Asp			
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gcc gag ttc tgc ggc cggt atc cac act cgc tac tca tcg gcc tac gag			672
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Leu Glu Gly Ala Val Lys Arg Ala Asp Leu Val Ile Gly Ala Val Leu			
225	230	235	240
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Val Pro Gly Ala Lys Ala Pro Lys Leu Val Ser Asn Ser Leu Val Ala			
245	250	255	
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His Met Lys Pro Gly Ala Val Leu Val Asp Ile Ala Ile Asp Gln Gly			
260	265	270	
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Gly Cys Phe Glu Gly Ser Arg Pro Thr Thr Tyr Asp His Pro Thr Phe			
275	280	285	
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Ala Val His Asp Thr Leu Phe Tyr Cys Val Ala Asn Met Pro Ala Ser			
290	295	300	
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Val Pro Lys Thr Ser Thr Tyr Ala Leu Thr Asn Ala Thr Met Pro Tyr			
305	310	315	320
gtg ctc gag ctt gcc gac cat ggc tgg cgg gcg tgc cgg tcg aat			1008
Val Leu Glu Leu Ala Asp His Gly Trp Arg Ala Ala Cys Arg Ser Asn			
325	330	335	
ccg gca cta gcc aaa ggt ctt tcg acg cac gaa ggg gcg tta ctg tcc			1056
Pro Ala Leu Ala Lys Gly Leu Ser Thr His Glu Gly Ala Leu Leu Ser			

340

345

350

gaa cggtg gcc acc gac ctgggg gtgcgc ttc acc gag ccc gcc agc 1104
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355 360 365

gtgtcgcc tga 1116
Val Leu Ala
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<210> 2
<211> 371
<212> PRT
<213> Mycobacterium tuberculosis

<220>
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<223> Sequence is identical to SwissProt entry SP:DHA_MYCTU

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Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45

Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60

Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80

Glu Tyr Gly Arg Leu Arg His Gly Gln Ile Leu Phe Thr Phe Leu His
85 90 95

Leu Ala Ala Ser Arg Ala Cys Thr Asp Ala Leu Leu Asp Ser Gly Thr
100 105 110

Thr Ser Ile Ala Tyr Glu Thr Val Gln Thr Ala Asp Gly Ala Leu Pro
115 120 125

Leu Leu Ala Pro Met Ser Glu Val Ala Gly Arg Leu Ala Ala Gln Val
130 135 140

Gly Ala Tyr His Leu Met Arg Thr Gln Gly Gly Arg Gly Val Leu Met
145 150 155 160

Gly Gly Val Pro Gly Val Glu Pro Ala Asp Val Val Val Ile Gly Ala
165 170 175

Gly Thr Ala Gly Tyr Asn Ala Ala Arg Ile Ala Asn Gly Met Gly Ala
180 185 190

Thr Val Thr Val Leu Asp Ile Asn Ile Asp Lys Leu Arg Gln Leu Asp
195 200 205

Ala Glu Phe Cys Gly Arg Ile His Thr Arg Tyr Ser Ser Ala Tyr Glu
210 215 220

Leu Glu Gly Ala Val Lys Arg Ala Asp Leu Val Ile Gly Ala Val Leu
225 230 235 240

Val Pro Gly Ala Lys Ala Pro Lys Leu Val Ser Asn Ser Leu Val Ala
245 250 255

His Met Lys Pro Gly Ala Val Leu Val Asp Ile Ala Ile Asp Gln Gly
260 265 270

Gly Cys Phe Glu Gly Ser Arg Pro Thr Thr Tyr Asp His Pro Thr Phe
275 280 285

Ala Val His Asp Thr Leu Phe Tyr Cys Val Ala Asn Met Pro Ala Ser
290 295 300

Val Pro Lys Thr Ser Thr Tyr Ala Leu Thr Asn Ala Thr Met Pro Tyr
305 310 315 320

Val Leu Glu Leu Ala Asp His Gly Trp Arg Ala Ala Cys Arg Ser Asn
325 330 335

Pro Ala Leu Ala Lys Gly Leu Ser Thr His Glu Gly Ala Leu Leu Ser
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Val Leu Ala
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gcc atc acc ccg gcc ggc gtc gcg gaa cta acc cgt cgt ggc cat gag		96
Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu		
20 25 30		
gtg ctc atc cag gca ggt gcc gga gag ggc tcg gct atc acc gac gcg		144
Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala		
35 40 45		
gat ttc aag gcg gca ggc gcg caa ctg gtc ggc acc gcc gac cag gtg		192
Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val		
50 55 60		
tgg gcc gac gct gat tta ttg ctc aag gtc aaa gaa ccg ata gcg gcg		240
Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala		
65 70 75 80		
gaa tac ggc cgc ctg cga cac ggg cga tct tgt tca cgt tct tgc att		288
Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile		
85 90 95		
tgg ccg cgt cac gtg ctt gca ccg atg cgt tgt tgg att ccg gca cca		336
Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro		
100 105 110		
cgt caa ttg cct acg aga ccg tcc aga ccg ccg acg gcg cac tac ccc		384
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Cys Leu Pro Arg		
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 1 5 10 15

Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
 20 25 30

Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
 35 40 45

Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
 50 55 60

Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
 65 70 75 80

Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile
 85 90 95

Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro
 100 105 110

Arg Gln Leu Pro Thr Arg Pro Ser Arg Pro Pro Thr Ala His Tyr Pro
 115 120 125

Cys Leu Pro Arg
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<210> 5
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 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
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 <222> (1)..(1386)
 <223> Sequence is identical to the complement of nucleotides 13172-14551
 of GenBank entry GB:MTV030 [AL021428]
 Sequence is identical to the complement of nucleotides 13195-14580
 of GenBank entry GB:AE006919

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 1 5 10 15

agt tcc cac acc gtg gga ccg atg cgc gcg gca aac cag ttc gta gtt 96
 Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Asn Gln Phe Val Val

20	25	30	
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gac ctg cat ccc gac atc gtt ctg cca acg cat ccc aac gga atg acg Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr 115	120	125	384
ttc act gcc gcg ggc cca cac ggc cgc gtc ttg gcc acc gag act tat Phe Thr Ala Ala Gly Pro His Gly Arg Val Leu Ala Thr Glu Thr Tyr 130	135	140	432
ttt tcg gtg ggc gga ggg ttc atc gtc acg gaa cag acc agc ggc aac Phe Ser Val Gly Gly Phe Ile Val Thr Glu Gln Thr Ser Gly Asn 145	150	155	480
agc ggc caa cat cca tgc tca gtt gcc ctt ccc tac gtg tcg gcc caa Ser Gly Gln His Pro Cys Ser Val Ala Leu Pro Tyr Val Ser Ala Gln 165	170	175	528
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gct ctg cgc aac gaa aca tgt tgc cgc acc gag aac gag gta cgc gcc Ala Leu Arg Asn Glu Thr Cys Cys Arg Thr Glu Asn Glu Val Arg Ala 195	200	205	624
gct ctg ctc cac ctg cgc gac gtc atg gtt gag tgc gaa cag cgg agc Ala Leu Leu His Leu Arg Asp Val Met Val Glu Cys Glu Gln Arg Ser 210	215	220	672
atc gct cgc gaa ggg ttg ctt cct ggc ggc ctc cgg gtg cgc cgg cga Ile Ala Arg Glu Gly Leu Leu Pro Gly Gly Leu Arg Val Arg Arg Arg 225	230	235	720
gct aag gtg tgg tat gac cgc ttg aac gcc gaa gac ccc act cgc aag Ala Lys Val Trp Tyr Asp Arg Leu Asn Ala Glu Asp Pro Thr Arg Lys 245	250	255	768

ccg gaa ttc gct gag gac tgg gtc aac ctg gtc gcg ctg gca gtc aac Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn 260	265	270	816
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tcg gcc ggc gcg ggg gac ccc gac gat gtc acc gtg cga ttc ctg ctc Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu 305	310	315	960
act gct gga gcc atc gga tcg ttg ttc aag gag cga gca tcg atc tcc Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser 325	330	335	1008
gga gcc gag gtc ggc tgt cag ggc gag gtc ggc tcc gcg gcc gcc atg Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ala Ala Met 340	345	350	1056
gcc gcc gca ttg gct gaa atc ctc ggc ggc aca ccg cga caa gtg Ala Ala Ala Gly Leu Ala Glu Ile Leu Gly Gly Thr Pro Arg Gln Val 355	360	365	1104
gaa aac gcc gcc gag atc gcc atg gaa cac agc ctc ggc ctg acc tgt Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys 370	375	380	1152
gac ccc atc gcc ggg ctg gtg cag atc ccc tgc atc gaa ccg aac gcg Asp Pro Ile Ala Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala 385	390	395	1200
att tcc gcc ggc aag gcc atc aac gcc gca cgg atg gca ttg cgc ggc Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly 405	410	415	1248
gac ggc atc cat cgc gtc acc ctc gac cag gtc atc gac acc atg cgc Asp Gly Ile His Arg Val Thr Leu Asp Gln Val Ile Asp Thr Met Arg 420	425	430	1296
gcc acc ggc gcg gac atg cac acc aag tac aag gaa acc tcg gcc ggc Ala Thr Gly Ala Asp Met His Thr Lys Tyr Lys Glu Thr Ser Ala Gly 435	440	445	1344
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<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221>

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<223> Sequence is identical to SwissProt entry SP:SDHL_MYCTU
Sequence is identical to GenBank entries GP:AE006919_13
and GP:MTV030_11

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20 25 30

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35 40 45

Asp Leu Phe Gly Ser Leu Ala Ala Thr Gly Ala Gly His Gly Thr Met
50 55 60

Ser Ala Ile Leu Leu Gly Leu Glu Gly Cys Gln Pro Glu Thr Ile Thr
65 70 75 80

Thr Glu His Lys Glu Arg Arg Leu Ala Glu Ile Ala Ala Ser Gly Val
85 90 95

Thr Arg Ile Gly Gly Val Ile Pro Val Pro Leu Thr Glu Arg Asp Ile
100 105 110

Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr
115 120 125

Phe Thr Ala Ala Gly Pro His Gly Arg Val Leu Ala Thr Glu Thr Tyr
130 135 140

Phe Ser Val Gly Gly Phe Ile Val Thr Glu Gln Thr Ser Gly Asn
145 150 155 160

Ser Gly Gln His Pro Cys Ser Val Ala Leu Pro Tyr Val Ser Ala Gln
165 170 175

Glu Leu Leu Asp Ile Cys Asp Arg Leu Asp Val Ser Ile Ser Glu Ala
180 185 190

Ala Leu Arg Asn Glu Thr Cys Cys Arg Thr Glu Asn Glu Val Arg Ala
195 200 205

Ala Leu Leu His Leu Arg Asp Val Met Val Glu Cys Glu Gln Arg Ser
210 215 220

Ile Ala Arg Glu Gly Leu Leu Pro Gly Gly Leu Arg Val Arg Arg Arg
225 230 235 240

Ala Lys Val Trp Tyr Asp Arg Leu Asn Ala Glu Asp Pro Thr Arg Lys
245 250 255

Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn
260 265 270

Glu Glu Asn Ala Ser Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly
275 280 285

Ala Ala Gly Ile Val Pro Ala Val Leu His Tyr Ala Ile His Tyr Thr
290 295 300

Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu
305 310 315 320

Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser
325 330 335

Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ala Ala Met
340 345 350

Ala Ala Ala Gly Leu Ala Glu Ile Leu Gly Gly Thr Pro Arg Gln Val
355 360 365

Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys
370 375 380

Asp Pro Ile Ala Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala
385 390 395 400

Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly
405 410 415

Asp Gly Ile His Arg Val Thr Leu Asp Gln Val Ile Asp Thr Met Arg
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<210> 7
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<212> DNA
<213> Mycobacterium tuberculosis

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<222> (1) .. (1437)
<223> Sequence is identical to GenBank entry GB:MTU87280 [U87280]
      Sequence is identical to nucleotides 163-1599 of GenBank
      entry GB:MTCY427 [Z70692]
      Sequence is identical to nucleotides 93-1529 of GenBank entry GB:AE00701
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 Lys Val Glu Tyr Val Asp Val Arg Phe Cys Asp Leu Pro Gly Ile Met
 20 25 30

 cag cac ttc acg att ccg gct tcg gcc ttt gac aag agc gtg ttt gac 144
 Gln His Phe Thr Ile Pro Ala Ser Ala Phe Asp Lys Ser Val Phe Asp
 35 40 45

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 His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile
 65 70 75 80

 gac ccg ttc cgc gcg gcc aag acg ctg aat atc aac ttc ttt gtg cac 288
 Asp Pro Phe Arg Ala Ala Lys Thr Leu Asn Ile Asn Phe Phe Val His
 85 90 95

 gac ccg ttc acc ctg gag ccg tac tcc cgc gac ccg cgc aac atc gcc 336
 Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala
 100 105 110

 cgc aag gcc gag aac tac ctg atc agc act ggc atc gcc gac acc gca 384

Arg Lys Ala Glu Asn Tyr Leu Ile Ser Thr Gly Ile Ala Asp Thr Ala		
115	120	125
tac ttc ggc gcc gag gcc gag ttc tac att ttc gat tcg gtg agc ttc		432
Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe		
130	135	140
gac tcg cgc gcc aac ggc tcc ttc tac gag gtg gac gcc atc tcg ggg		480
Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly		
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Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg		
165	170	175
ggc tac aag gtc cgc cac aag ggc ggg tat ttc cca gtg gcc ccc aac		576
Gly Tyr Lys Val Arg His Lys Gly Tyr Phe Pro Val Ala Pro Asn		
180	185	190
gac caa tac gtc gac ctg cgc gac aag atg ctg acc aac ctg atc aac		624
Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn		
195	200	205
tcc ggc ttc atc ctg gag aag ggc cac cac gag gtg ggc agc ggc gga		672
Ser Gly Phe Ile Leu Glu Lys Gly His His Glu Val Gly Ser Gly Gly		
210	215	220
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Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp		
225	230	235
240		
gac atg cag ttg tac aag tac atc atc aag aac acc gcc tgg cag aac		768
Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn		
245	250	255
ggc aaa acg gtc acg ttc atg ccc aag ccg ctg ttc ggc gac aac ggg		816
Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly		
260	265	270
tcc ggc atg cac tgt cat cag tcg ctg tgg aag gac ggg gcc ccg ctg		864
Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu		
275	280	285
atg tac gac gag acg ggt tat gcc ggt ctg tcg gac acg gcc cgt cat		912
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290	295	300
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Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr		
305	310	315
320		
aac ccg acg gtg aac tcc tac aag cgg ctg gtt ccc ggt tac gag gcc		1008
Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala		
325	330	335
ccg atc aac ctg gtc tat agc cag cgc aac cgg tcg gca tgc gtg cgc		1056
Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Cys Val Arg		

340	345	350		
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agc ccc gac tcg tcg ggc aac ccg tat ctg gcg ttc tcg gcc atg ctg Ser Pro Asp Ser Ser Gly Asn Pro Tyr Leu Ala Phe Ser Ala Met Leu 370	375	380	1152	
atg gca ggc ctg gac ggt atc aag aac aag atc gag ccg cag gcg ccc Met Ala Gly Leu Asp Gly Ile Lys Asn Lys Ile Glu Pro Gln Ala Pro 385	390	395	400	1200
gtc gac aag gat ctc tac gag ctg ccg gaa gag gcc gcg agt atc Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile 405	410	415	1248	
ccg cag act ccg acc cag ctg tca gat gtg atc gac cgt ctc gag gcc Pro Gln Thr Pro Thr Gln Leu Ser Asp Val Ile Asp Arg Leu Glu Ala 420	425	430	1296	
gac cac gaa tac ctc acc gaa gga ggg gtg ttc aca aac gac ctg atc Asp His Glu Tyr Leu Thr Glu Gly Val Phe Thr Asn Asp Leu Ile 435	440	445	1344	
gag acg tgg atc agt ttc aag cgc gaa aac gag atc gag ccg gtc aac Glu Thr Trp Ile Ser Phe Lys Arg Glu Asn Glu Ile Glu Pro Val Asn 450	455	460	1392	
atc cgg ccg cat ccc tac gaa ttc gcg ctg tac tac gac gtt taa Ile Arg Pro His Pro Tyr Glu Phe Ala Leu Tyr Tyr Asp Val 465	470	475	1437	
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35

40

45

Asp Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Gln Ser Ile
50 55 60

His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile
65 70 75 80

Asp Pro Phe Arg Ala Ala Lys Thr Leu Asn Ile Asn Phe Phe Val His
85 90 95

Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala
100 105 110

Arg Lys Ala Glu Asn Tyr Leu Ile Ser Thr Gly Ile Ala Asp Thr Ala
115 120 125

Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe
130 135 140

Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly
145 150 155 160

Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg
165 170 175

Gly Tyr Lys Val Arg His Lys Gly Gly Tyr Phe Pro Val Ala Pro Asn
180 185 190

Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn
195 200 205

Ser Gly Phe Ile Leu Glu Lys Gly His His Glu Val Gly Ser Gly Gly
210 215 220

Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp
225 230 235 240

Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn
245 250 255

Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly
260 265 270

Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu
275 280 285

Met Tyr Asp Glu Thr Gly Tyr Ala Gly Leu Ser Asp Thr Ala Arg His
290 295 300

Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr
305 310 315 320

Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala
325 330 335

Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Cys Val Arg
340 345 . 350

Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Leu Glu Phe Arg
355 360 365

Ser Pro Asp Ser Ser Gly Asn Pro Tyr Leu Ala Phe Ser Ala Met Leu
370 375 380 . .

Met Ala Gly Leu Asp Gly Ile Lys Asn Lys Ile Glu Pro Gln Ala Pro
385 390 395 400

Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile
405 410 415

Pro Gln Thr Pro Thr Gln Leu Ser Asp Val Ile Asp Arg Leu Glu Ala
420 425 430

Asp His Glu Tyr Leu Thr Glu Gly Gly Val Phe Thr Asn Asp Leu Ile
435 440 445

Glu Thr Trp Ile Ser Phe Lys Arg Glu Asn Glu Ile Glu Pro Val Asn
450 455 460

Ile Arg Pro His Pro Tyr Glu Phe Ala Leu Tyr Tyr Asp Val
465 470 475

<210> 9
<211> 1341
<212> DNA

<213> *Mycobacterium tuberculosis*

<220>

<221> CDS

<222> (1)..(1341)

<223> Sequence is identical to complement of nucleotides 4950-6290 of GenBank entry GB:MTCY427 [Z70692]

Sequence is identical to complement of nucleotides 4880-6220 of GenBank entry GB:AE007073

<400> 9

atg gac cga cag aag gaa ttc gtt ctt cgt acc ctg gaa gaa cgc gac	48
Met Asp Arg Gln Lys Glu Phe Val Leu Arg Thr Leu Glu Glu Arg Asp	
1 5 10 15	

atc cgc ttc gtc cg ^g ctg tgg ttc aca gac gtg ctc ggt ttc ctc aag	96
Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys	
20 25 30	

tcg gtc gcc atc gcc cca gcc gaa ctc gag ggc gcc ttc gag gaa ggc	144
Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly	
35 40 45	

atc ggc ttc gac gga tcc tcg atc gag ggc ttt gcg cgg gtc tcg gaa	192
Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu	
50 55 60	

tcc gat acg gtg gc ^g cac cc ^g gac cc ^g tcg acc ttc cag gtg ctg ccc	240
Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro	
65 70 75 80	

tgg gcc acc agt tcc ggc cac cac tca gc ^g cgg atg ttt tgc gac	288
Trp Ala Thr Ser Ser Gly His His Ser Ala Arg Met Phe Cys Asp	
85 90 95	

atc acc atg cc ^g gac ggc tcg cc ^g tcg tgg gc ^g gac cc ^g cgg cac gtg	336
Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val	
100 105 110	

ttg cgg cgg cag ctg acg aag gcc ggc gaa ctc ggc ttc tcc tgc tac	384
Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr	
115 120 125	

gtg cat ccc gaa atc gag ttc ttc ctg ctc aag ccc gga ccc gag gac	432
Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp	
130 135 140	

ggg tcg gtg ccc gtc cc ^g gtc gac aac gcc ggc tat ttc gac caa gc ^g	480
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala	
145 150 155 160	

gtg cac gac tcc gcc ttg aac ttt cgc cgc cac gc ^g atc gat gcc ctg	528
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu	
165 170 175	

gaa ttc atg ggc atc tcg gtg gag ttc agc cat cac gaa ggc gca ccc	576
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Glu	Phe	Met	Gly	Ile	Ser	Val	Glu	Phe	Ser	His	His	Glu	Gly	Ala	Pro		
180							185					190					
ggc	cag	cag	gag	atc	gac	ctg	cggttt	gcc	gac	gct	ctg	tcg	atg	gct		624	
Gly	Gln	Gln	Glu	Ile	Asp	Leu	Arg	Phe	Ala	Asp	Ala	Leu	Ser	Met	Ala		
195							200					205					
gac	aac	gtg	atg	acc	tcc	cgc	tac	gtc	atc	aaa	gaa	gtc	gct	ctg	gaa		672
Asp	Asn	Val	Met	Thr	Phe	Arg	Tyr	Val	Ile	Lys	Glu	Val	Ala	Leu	Glu		
210							215				220						
gag	ggc	gcc	cggttt	gct	atg	ccc	aag	cca	tcc	ggc	cag	cac	ccg			720	
Glu	Gly	Ala	Arg	Ala	Ser	Phe	Met	Pro	Lys	Pro	Phe	Gly	Gln	His	Pro		
225							230			235			240				
ggc	tcg	gct	atg	acc	cac	atg	agc	ctg	tcc	gag	ggt	gat	gtc	aac		768	
Gly	Ser	Ala	Met	His	Thr	His	Met	Ser	Leu	Phe	Glu	Gly	Asp	Val	Asn		
245							250			255							
gct	tcc	cac	agc	gct	gat	ccg	ctg	cag	ctg	tcg	gaa	gtg	ggt	aaa		816	
Ala	Phe	His	Ser	Ala	Asp	Asp	Pro	Leu	Gln	Leu	Ser	Glu	Val	Gly	Lys		
260							265			270							
tcg	tcc	atc	gcc	ggg	atc	ctg	gag	cac	gct	tgc	gag	atc	agc	gct		864	
Ser	Phe	Ile	Ala	Gly	Ile	Leu	Glu	His	Ala	Cys	Glu	Ile	Ser	Ala	Val		
275							280			285							
aca	aat	cag	tgg	gtc	aac	tct	tac	aag	cggttt	ctg	gtg	cag	ggc	ggc	gaa		912
Thr	Asn	Gln	Trp	Val	Asn	Ser	Tyr	Lys	Arg	Leu	Val	Gln	Gly	Gly	Glu		
290							295			300							
gct	ccc	acg	gcc	gct	tcc	tgg	ggg	gcc	gcc	aac	cga	tcc	gcc	cta	gtg		960
Ala	Pro	Thr	Ala	Ala	Ser	Trp	Gly	Ala	Ala	Asn	Arg	Ser	Ala	Leu	Val		
305							310			315			320				
cggttt	ccg	atg	tac	acg	ccg	cac	aag	acc	tcg	tcg	cggttt	cggttt	gtc	gaa		1008	
Arg	Val	Pro	Met	Tyr	Thr	Pro	His	Lys	Thr	Ser	Ser	Arg	Arg	Arg	Val	Glu	
325							330			335							
gtatcg	cgc	agc	cct	gat	tcg	gct	aat	ccc	tat	ctg	aca	ttc	gcc	gtg		1056	
Val	Arg	Ser	Pro	Asp	Ser	Ala	Cys	Asn	Pro	Tyr	Leu	Thr	Phe	Ala	Val		
340							345			350							
ctg	ctg	gcc	gct	ttt	cggttt	gtatcg	gat	aag	ggt	tac	gtg	ctg	ggc			1104	
Leu	Leu	Ala	Ala	Gly	Leu	Arg	Gly	Val	Glu	Lys	Gly	Tyr	Val	Leu	Gly		
355							360			365							
ccg	cag	gcc	gag	gac	aac	gtatcg	tgg	gac	ctc	aca	ccc	gag	gaa	cgc	cga		1152
Pro	Gln	Ala	Glu	Asp	Asn	Val	Trp	Asp	Leu	Thr	Pro	Glu	Glu	Arg	Arg		
370							375			380							
gct	atg	ggg	tac	cga	gaa	ttt	cggttt	tcc	agt	ttt	gat	agt	gtc	ctg	cgc		1200
Ala	Met	Gly	Tyr	Arg	Glu	Leu	Pro	Ser	Ser	Leu	Asp	Ser	Ala	Leu	Arg		
385							390			395			400				
gcc	atg	gag	gcc	tcc	gaa	ctc	gtc	gct	gag	gcc	ttt	ggg	gag	cac	gtt		1248
Ala	Met	Glu	Ala	Ser	Glu	Leu	Val	Ala	Glu	Ala	Leu	Gly	Glu	His	Val		

405

410

415

ttt gac ttt ttc ttg cgc aac aag cgc acg gag tgg gcg aac tac cgc 1296
 Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
 420 425 430

agc cac gtc acg cca tac gag ctg cgc acc tac ctg tcg ctg tag 1341
 Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
 435 440 445

<210> 10

<211> 446

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221>

<222>

<223> Sequence is identical to SwissProt entry SP:GLN2_MYCTU
 Sequence is identical to PIR entry PIR:B70776

<400> 10

Met Asp Arg Gln Lys Glu Phe Val Leu Arg Thr Leu Glu Glu Arg Asp
 1 5 10 15

Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys
 20 25 30

Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly
 35 40 45

Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu
 50 55 60

Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
 65 70 75 80

Trp Ala Thr Ser Ser Gly His His Ser Ala Arg Met Phe Cys Asp
 85 90 95

Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val
 100 105 110

Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr
 115 120 125

Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp

130	135	140
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala		
145	150	155
160		
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu		
165	170	175
Glu Phe Met Gly Ile Ser Val Glu Phe Ser His His Glu Gly Ala Pro		
180	185	190
Gly Gln Gln Glu Ile Asp Leu Arg Phe Ala Asp Ala Leu Ser Met Ala		
195	200	205
Asp Asn Val Met Thr Phe Arg Tyr Val Ile Lys Glu Val Ala Leu Glu		
210	215	220
Glu Gly Ala Arg Ala Ser Phe Met Pro Lys Pro Phe Gly Gln His Pro		
225	230	235
240		
Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Val Asn		
245	250	255
Ala Phe His Ser Ala Asp Asp Pro Leu Gln Leu Ser Glu Val Gly Lys		
260	265	270
Ser Phe Ile Ala Gly Ile Leu Glu His Ala Cys Glu Ile Ser Ala Val		
275	280	285
Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Leu Val Gln Gly Gly Glu		
290	295	300
Ala Pro Thr Ala Ala Ser Trp Gly Ala Ala Asn Arg Ser Ala Leu Val		
305	310	315
320		
Arg Val Pro Met Tyr Thr Pro His Lys Thr Ser Ser Arg Arg Val Glu		
325	330	335
Val Arg Ser Pro Asp Ser Ala Cys Asn Pro Tyr Leu Thr Phe Ala Val		
340	345	350
Leu Leu Ala Ala Gly Leu Arg Gly Val Glu Lys Gly Tyr Val Leu Gly		
355	360	365

Pro Gln Ala Glu Asp Asn Val Trp Asp Leu Thr Pro Glu Glu Arg Arg
 370 375 380

Ala Met Gly Tyr Arg Glu Leu Pro Ser Ser Leu Asp Ser Ala Leu Arg
 385 390 395 400

Ala Met Glu Ala Ser Glu Leu Val Ala Glu Ala Leu Gly Glu His Val
 405 410 415

Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
 420 425 430

Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
 435 440 445

<210> 11

<211> 1353

<212> DNA

<213> *Mycobacterium tuberculosis*

<220>

<221> CDS

<222> (1) .. (1353)

<223> Sequence is identical to nucleotides 4871-6223

of GenBank entry GB:MTCY180 [Z97193]

Sequence is identical to nucleotides 7308-8660

of GenBank entry GB:AE007049

<400> 11

atg aca gcc aca ccg ctt gcc gcg gcc gcg atc gcc caa ttg gag gca
 Met Thr Ala Thr Pro Leu Ala Ala Ala Ile Ala Gln Leu Glu Ala
 1 5 10 15

48

gag ggc gtc gac acc gtc atc ggc acc gtc gtg aac ccc gcc gga ctc
 Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu
 20 25 30

96

acc cag gcc aag acc gtg ccg ata cgc cg acc aac aca ttc gcc aat
 Thr Gln Ala Lys Thr Val Pro Ile Arg Arg Thr Asn Thr Phe Ala Asn
 35 40 45

144

cct ggc ctc ggc gcc agt ccg gtg tgg cat acc ttc tgt atc gac caa
 Pro Gly Leu Gly Ala Ser Pro Val Trp His Thr Phe Cys Ile Asp Gln
 50 55 60

192

tgc agt att gca ttc acc gca gac atc agt gtg gtc ggc gat caa cgt
 Cys Ser Ile Ala Phe Thr Ala Asp Ile Ser Val Val Gly Asp Gln Arg
 65 70 75 80

240

ctc	cgc	atc	gat	ctg	tcc	gcc	ttg	cgc	atc	atc	ggc	gac	ggg	ttg	gcg		288
Leu	Arg	Ile	Asp	Leu	Ser	Ala	Leu	Arg	Ile	Ile	Gly	Asp	Gly	Leu	Ala		
				85					90					95			
tgg	gcg	ccc	gcc	ggg	ttc	ttc	gag	cag	gac	ggc	aca	ccg	gtc	ccc	gcc		336
Trp	Ala	Pro	Ala	Gly	Phe	Phe	Glu	Gln	Asp	Gly	Thr	Pro	Val	Pro	Ala		
				100				105				110					
tgc	agc	cga	gga	aca	ctg	agc	cg	atc	gag	gcc	g	ctt	gct	gat	gcc		384
Cys	Ser	Arg	Gly	Thr	Leu	Ser	Arg	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Ala		
				115				120				125					
ggc	atc	gac	g	gta	atc	ggc	cac	gaa	gtc	gaa	ttc	ctc	ttg	gtc	gac		432
Gly	Ile	Asp	Ala	Val	Ile	Gly	His	Glu	Val	Glu	Phe	Leu	Leu	Val	Asp		
				130			135			140							
gcg	gac	ggc	cag	cg	ctg	cct	tcg	acg	ctg	tgg	g	cag	tac	ggt	gtc		480
Ala	Asp	Gly	Gln	Arg	Leu	Pro	Ser	Thr	Leu	Trp	Ala	Gln	Tyr	Gly	Val		
				145			150		155		160						
gcc	ggg	gtg	ctc	gag	cac	gag	g	ttc	gtc	cg	gat	gtc	aac	gcc	g		528
Ala	Gly	Val	Leu	Glu	His	Glu	Ala	Phe	Val	Arg	Asp	Val	Asn	Ala	Ala		
				165			170			175							
gca	acg	gca	gca	ggc	atc	gct	atc	gag	cag	ttc	cat	ccc	gaa	tac	ggt		576
Ala	Thr	Ala	Ala	Gly	Ile	Ala	Ile	Glu	Gln	Phe	His	Pro	Glu	Tyr	Gly		
				180			185			190							
gcc	aac	caa	ttc	gag	atc	tcg	tta	g	ccg	cag	ccg	ccg	gtc	g	cc		624
Ala	Asn	Gln	Phe	Glu	Ile	Ser	Leu	Ala	Pro	Gln	Pro	Pro	Val	Ala	Ala		
				195			200		205								
gcc	gat	cag	ctg	gtg	ctg	acc	cg	ctc	atc	atc	ggc	cgt	acc	gcc	cg		672
Ala	Asp	Gln	Leu	Val	Leu	Thr	Arg	Leu	Ile	Ile	Gly	Arg	Thr	Ala	Arg		
				210			215			220							
cg	cac	ggg	tta	cg	gtg	agc	cta	tcg	cca	g	ccc	ttc	gcc	g	gt		720
Arg	His	Gly	Leu	Arg	Val	Ser	Leu	Ser	Pro	Ala	Pro	Phe	Ala	Gly	Ser		
				225			230		235			240					
atc	gga	tcc	ggt	gcc	cac	caa	cac	ttc	tcg	ctg	act	atg	tcg	gaa	ggg		768
Ile	Gly	Ser	Gly	Ala	His	Gln	His	Phe	Ser	Leu	Thr	Met	Ser	Glu	Gly		
				245			250			255							
atg	ctg	ttc	tcc	ggt	ggg	act	gga	gca	gct	ggc	atg	acc	tcg	gcc	ggg		816
Met	Leu	Phe	Ser	Gly	Gly	Thr	Gly	Ala	Ala	Gly	Met	Thr	Ser	Ala	Gly		
				260			265			270							
gag	gcc	cg	gtg	gca	gga	gtg	ctt	cg	gga	cta	ccg	gac	gcc	caa	ggc		864
Glu	Ala	Ala	Val	Ala	Gly	Val	Leu	Arg	Gly	Leu	Pro	Asp	Ala	Gln	Gly		
				275			280			285							
atc	ctg	tgc	gga	tcg	atc	gtg	tcc	ggt	ctg	cga	atg	cga	ccc	ggt	aa		912
Ile	Leu	Cys	Gly	Ser	Ile	Val	Ser	Gly	Leu	Arg	Met	Arg	Pro	Gly	Asn		
				290			295			300							
tgg	gcc	gga	atc	tat	gca	tgc	tgg	ggt	acc	gaa	aa	cgg	gaa	g	cg		960

Trp Ala Gly Ile Tyr Ala Cys Trp Gly Thr Glu Asn Arg Glu Ala Ala			
305	310	315	320
gtg cga ttc gtc aag ggc ggg gct ggc agc gcg tac ggc ggg aac gtg			1008
Val Arg Phe Val Lys Gly Gly Ala Gly Ser Ala Tyr Gly Gly Asn Val			
325	330	335	
gag gtg aag gtc gtc gac ccg tcg gcc aac ccg tat ctc gcg tcg gcg			1056
Glu Val Lys Val Val Asp Pro Ser Ala Asn Pro Tyr Leu Ala Ser Ala			
340	345	350	
gcg atc ctc gga ctg gca ctc gac ggc atg aag acc aag gcg gtg ttg			1104
Ala Ile Leu Gly Leu Ala Leu Asp Gly Met Lys Thr Lys Ala Val Leu			
355	360	365	
ccg tcg gaa acg acc gta gac ccg aca cag ctg tct gac gtg gat cgt			1152
Pro Ser Glu Thr Thr Val Asp Pro Thr Gln Leu Ser Asp Val Asp Arg			
370	375	380	
gac cgt gcc ggc att ctg cga ctt gct gcc gat cag gcg gat gca att			1200
Asp Arg Ala Gly Ile Leu Arg Leu Ala Ala Asp Gln Ala Asp Ala Ile			
385	390	395	400
gct gta ctg gat agt tcg aaa ctg ctt cg ^t atc ctt ggc gat ccc			1248
Ala Val Leu Asp Ser Ser Lys Leu Leu Arg Cys Ile Leu Gly Asp Pro			
405	410	415	
gtg gta gat gcc gtc gcg gta cgc cag tta gag cat gag gc ^c tac			1296
Val Val Asp Ala Val Val Ala Val Arg Gln Leu Glu His Glu Arg Tyr			
420	425	430	
ggt gac ctc gat cct gc ^c cag ctg gcc gac aag ttc cg ^t atg gct tg ^t			1344
Gly Asp Leu Asp Pro Ala Gln Leu Ala Asp Lys Phe Arg Met Ala Trp			
435	440	445	
agt gtg taa			1353
Ser Val			
450			

<210> 12
<211> 450
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221>
<222>
<223> Sequence is identical to PIR entry PIR:C70515

<400> 12
Met Thr Ala Thr Pro Leu Ala Ala Ala Ile Ala Gln Leu Glu Ala
1 5 10 15

Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu

20

25

30

Thr Gln Ala Lys Thr Val Pro Ile Arg Arg Thr Asn Thr Phe Ala Asn
35 40 45

Pro Gly Leu Gly Ala Ser Pro Val Trp His Thr Phe Cys Ile Asp Gln
50 55 60

Cys Ser Ile Ala Phe Thr Ala Asp Ile Ser Val Val Gly Asp Gln Arg
65 70 75 80

Leu Arg Ile Asp Leu Ser Ala Leu Arg Ile Ile Gly Asp Gly Leu Ala
85 90 95

Trp Ala Pro Ala Gly Phe Phe Glu Gln Asp Gly Thr Pro Val Pro Ala
100 105 110

Cys Ser Arg Gly Thr Leu Ser Arg Ile Glu Ala Ala Leu Ala Asp Ala
115 120 125

Gly Ile Asp Ala Val Ile Gly His Glu Val Glu Phe Leu Leu Val Asp
130 135 140

Ala Asp Gly Gln Arg Leu Pro Ser Thr Leu Trp Ala Gln Tyr Gly Val
145 150 155 160

Ala Gly Val Leu Glu His Glu Ala Phe Val Arg Asp Val Asn Ala Ala
165 170 175

Ala Thr Ala Ala Gly Ile Ala Ile Glu Gln Phe His Pro Glu Tyr Gly
180 185 190

Ala Asn Gln Phe Glu Ile Ser Leu Ala Pro Gln Pro Pro Val Ala Ala
195 200 205

Ala Asp Gln Leu Val Leu Thr Arg Leu Ile Ile Gly Arg Thr Ala Arg
210 215 220

Arg His Gly Leu Arg Val Ser Leu Ser Pro Ala Pro Phe Ala Gly Ser
225 230 235 240

Ile Gly Ser Gly Ala His Gln His Phe Ser Leu Thr Met Ser Glu Gly
245 250 255

Met Leu Phe Ser Gly Gly Thr Gly Ala Ala Gly Met Thr Ser Ala Gly
260 265 270

Glu Ala Ala Val Ala Gly Val Leu Arg Gly Leu Pro Asp Ala Gln Gly
275 280 285

Ile Leu Cys Gly Ser Ile Val Ser Gly Leu Arg Met Arg Pro Gly Asn
290 295 300

Trp Ala Gly Ile Tyr Ala Cys Trp Gly Thr Glu Asn Arg Glu Ala Ala
305 310 315 320

Val Arg Phe Val Lys Gly Gly Ala Gly Ser Ala Tyr Gly Gly Asn Val
325 330 335

Glu Val Lys Val Val Asp Pro Ser Ala Asn Pro Tyr Leu Ala Ser Ala
340 345 350

Ala Ile Leu Gly Leu Ala Leu Asp Gly Met Lys Thr Lys Ala Val Leu
355 360 365

Pro Ser Glu Thr Thr Val Asp Pro Thr Gln Leu Ser Asp Val Asp Arg
370 375 380

Asp Arg Ala Gly Ile Leu Arg Leu Ala Ala Asp Gln Ala Asp Ala Ile
385 390 395 400

Ala Val Leu Asp Ser Ser Lys Leu Leu Arg Cys Ile Leu Gly Asp Pro
405 410 415

Val Val Asp Ala Val Val Ala Val Arg Gln Leu Glu His Glu Arg Tyr
420 425 430

Gly Asp Leu Asp Pro Ala Gln Leu Ala Asp Lys Phe Arg Met Ala Trp
435 440 445

Ser Val
450

<210> 13
<211> 1374
<212> DNA

<213> *Mycobacterium tuberculosis*

<220>

<221> CDS

<222> (1)..(1374)

<223> Sequence is identical to complement of nucleotides 3104-4477
of GenBank entry GB:MTV003 [AL008883]

Sequence is identical to complement of nucleotides 3138-4511
of GenBank entry GB:AE007117

<400> 13

gtg acc ggc ccc ggt tcg ccg ccg ttg gcg tgg acc gag ttg gag cga 48

Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
1 5 10 15

ctg gtc gcg gcc ggt gac gtc gac acc gtc atc gtc gcg ttc acc gac 96

Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
20 25 30

atg cag ggc cgg ctg gcc ggc aaa cgg ata tcg ggc cgg cat ttc gtc 144

Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val

35 40 45

gac gac ata gcc acc cgc ggc gtc gag tgc tgc agt tat ctg ctg gcc 192

Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala

50 55 60

gtg gac gtc gac ctg aac acg gtg ccc ggc tat gcg atg gcc agt tgg 240

Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp

65 70 75 80

gac acc ggc tac ggc gat atg gtg atg acg ccg gac ttg tcc act ctg 288

Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu

85 90 95

cgg ctg att cct tgg cta ccg gga acg gcg ctg gtg atc gcc gac ctg 336

Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu

100 105 110

gtc tgg gcc gac ggc agc gag gtc gcc tgc ccg cgc agc att ctg 384

Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu

115 120 125

cgc cgt cag ctc gat cgg ctc aag gcg cgc gga ctg gtc gcc gat gtg 432

Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val

130 135 140

gcc acc gag ctg gag ttc atc gtg ttc gac cag ccg tat cgc cag gca 480

Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala

145 150 155 160

tgg gcc agc ggg tat cgc ggg ctg acc ccg gcc agc gac tac aac atc 528

Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile

165 170 175

gac tac gcg ata ttg gca tcc tcg cgg atg gag ccg ttg ctg cgc gac 576

Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp			
180	185	190	
atc cgg ttg ggt atg gcc ggt gcg ggt ctg cga ttc gag gcg gtc aaa		624	
Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys			
195	200	205	
ggc gaa tgc aac atg ggc cag cag gag atc ggg ttt cgt tac gac gag		672	
Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu			
210	215	220	
gcg ctg gtc acc tgc gac aac cat gcg atc tac aag aac ggc gcc aag		720	
Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys			
225	230	235	240
gaa atc gcc gac cag cac ggc aag agc cta acg ttc atg gcg aaa tac		768	
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr			
245	250	255	
gat gaa cgc gaa ggt aat agc tgt cac atc cat gtc tcg ctg cgt ggc		816	
Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly			
260	265	270	
acg gat ggc tcc gcg gtg ttt gcc gac agt aac ggg ccg cac ggc atg		864	
Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met			
275	280	285	
tcg tcg atg ttc cgc agc ttc gtc gcc ggc cag ttg gcc acg ttg cgc		912	
Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg			
290	295	300	
gaa ttc acg ctg tgc tat gcg ccg acc att aac tcc tac aag cga ttt		960	
Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe			
305	310	315	320
gcc gat agc agt ttc gcg ccg acg gcg ctg gct tgg ggg ctg gac aat		1008	
Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn			
325	330	335	
cgc acc tgc gcc ctg cgg gtg gtt ggc cac ggg caa aac atc cgg gtc		1056	
Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val			
340	345	350	
gaa tgc cgg gtt ccc ggc ggt gat gtc aac cag tac ctg gcg gtg gcg		1104	
Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala			
355	360	365	
gct ctc att gct gga ggg ttg tac ggt atc gag cgg ggc ctt cag ctg		1152	
Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu			
370	375	380	
ccc gag ccc tgt gtc ggc aac gcc tac caa ggc gcc gat gtc gaa cgg		1200	
Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg			
385	390	395	400
ctg ccg gtt acg ctg gcc gac gcc gcg gtg ctg ttc gag gat tct gcg		1248	
Leu Pro Val Thr Leu Ala Asp Ala Val Leu Phe Glu Asp Ser Ala			

405

410

415

ctg gtg cgc gag gcg ttc ggc gag gat gtt gtc gcg cac tac ctg aac 1296
 Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
 420 425 430

aac gcg cgt gtg gag ctg gcg gcg ttc aac gcg gcg gtc acc gat tgg 1344
 Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
 435 440 445

gag agg ata cgt gga ttt gag cgc ctc tag 1374
 Glu Arg Ile Arg Gly Phe Glu Arg Leu
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<211> 457

<212> PRT

<213> Mycobacterium tuberculosis

<220>
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<223> Sequence is identical to PIR entry PIR:F70885

<400> 14
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Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
 20 25 30

Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
 35 40 45

Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
 50 55 60

Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
 65 70 75 80

Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
 85 90 95

Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
 100 105 110

Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
 115 120 125

Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
130 135 140

Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
145 150 155 160

Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
165 170 175

Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
180 185 190

Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
195 200 205

Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
210 215 220

Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
225 230 235 240

Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
245 250 255

Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
260 265 270

Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
275 280 285

Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
290 295 300

Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
305 310 315 320

Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
325 330 335

Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
340 345 350

Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
355 360 365

Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
370 375 380

Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
385 390 395 400

Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
405 410 415

Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
420 425 430

Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
435 440 445

Glu Arg Ile Arg Gly Phe Glu Arg Leu
450 455